



08/30/02

FIG. 1A

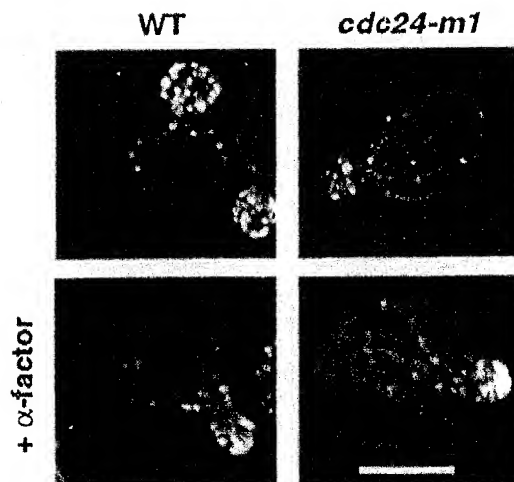


FIG. 1B

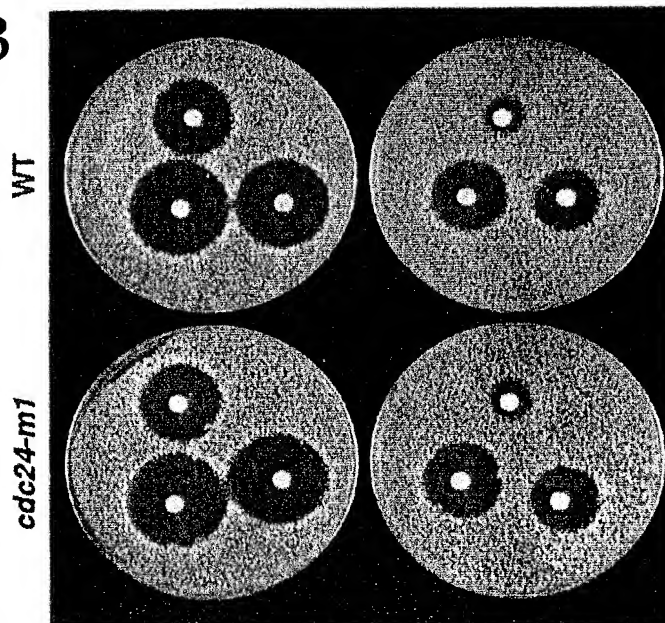
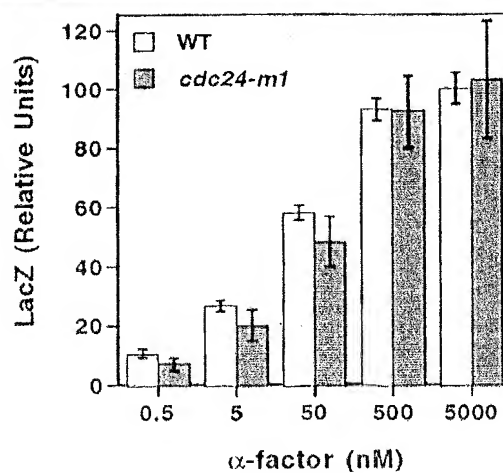


FIG. 1C





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FIG. 2A

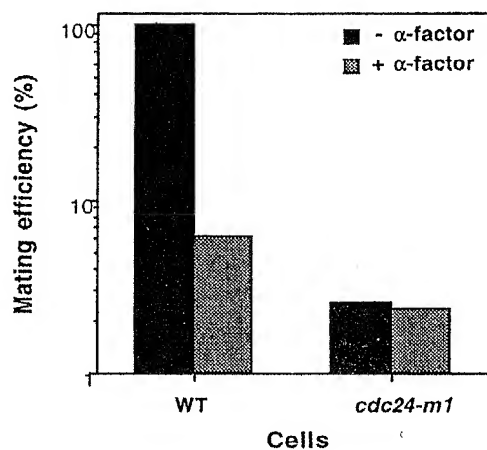


FIG. 2B

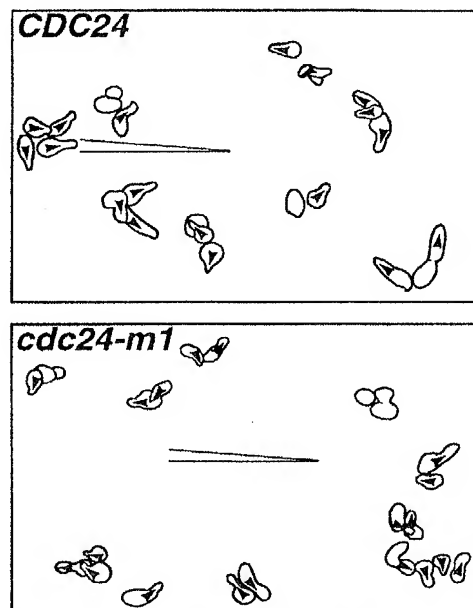


FIG. 2C

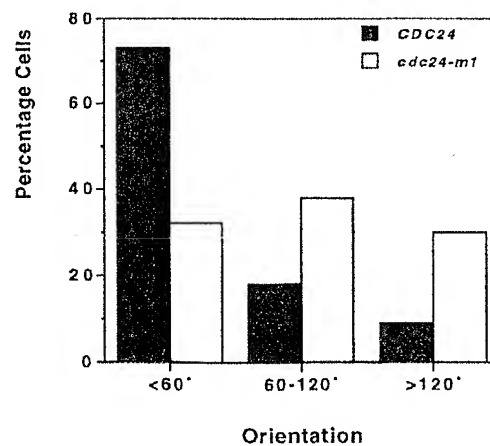
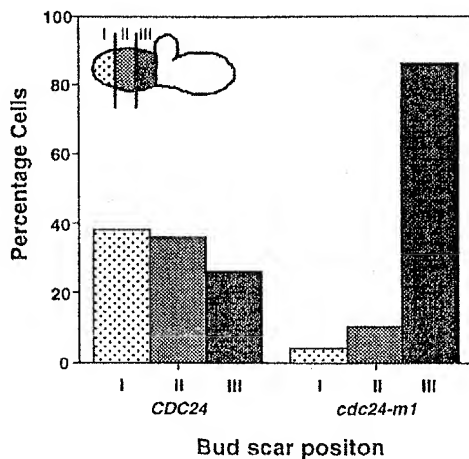


FIG. 3A

Cdc24-m1			QFKLPVIAFDLKVCKKSI	
Cdc24-m2			QFKLPVIASGLKVCKKSI	
Cdc24-m3			QFKLPVIAFDLKVCKKSI	
Cdc24 Sc	181		QFKLPVIASDLKVCKKSI	199
			
Dbl Hu	385		QYEFDVLLSPDLKVQMKTI	403

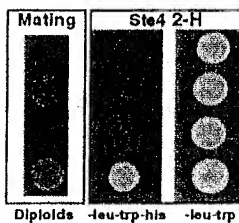


FIG. 3B

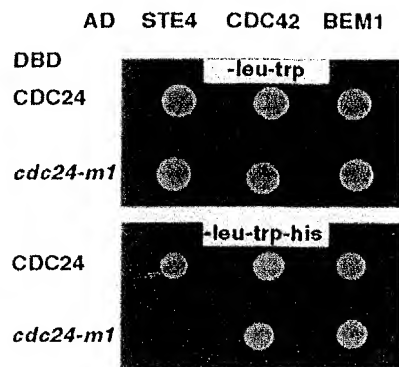


FIG. 3C

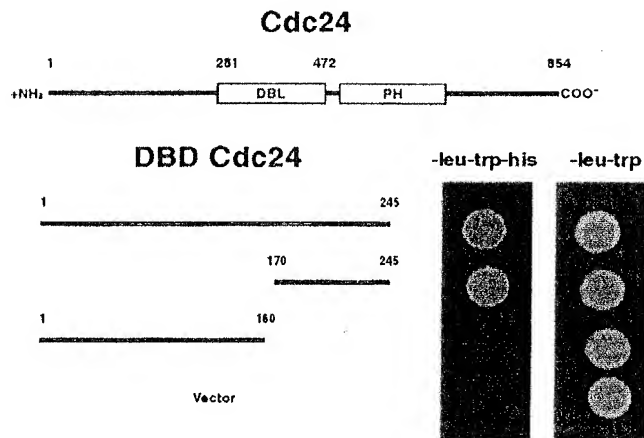
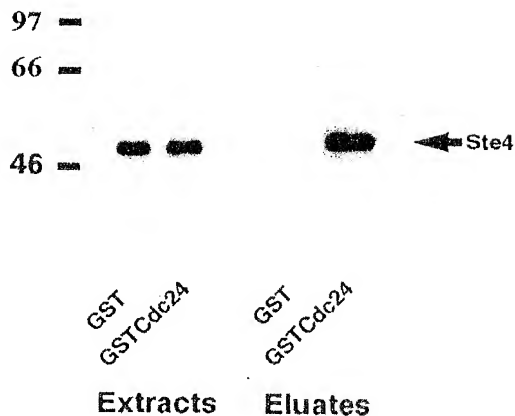


FIG. 3D





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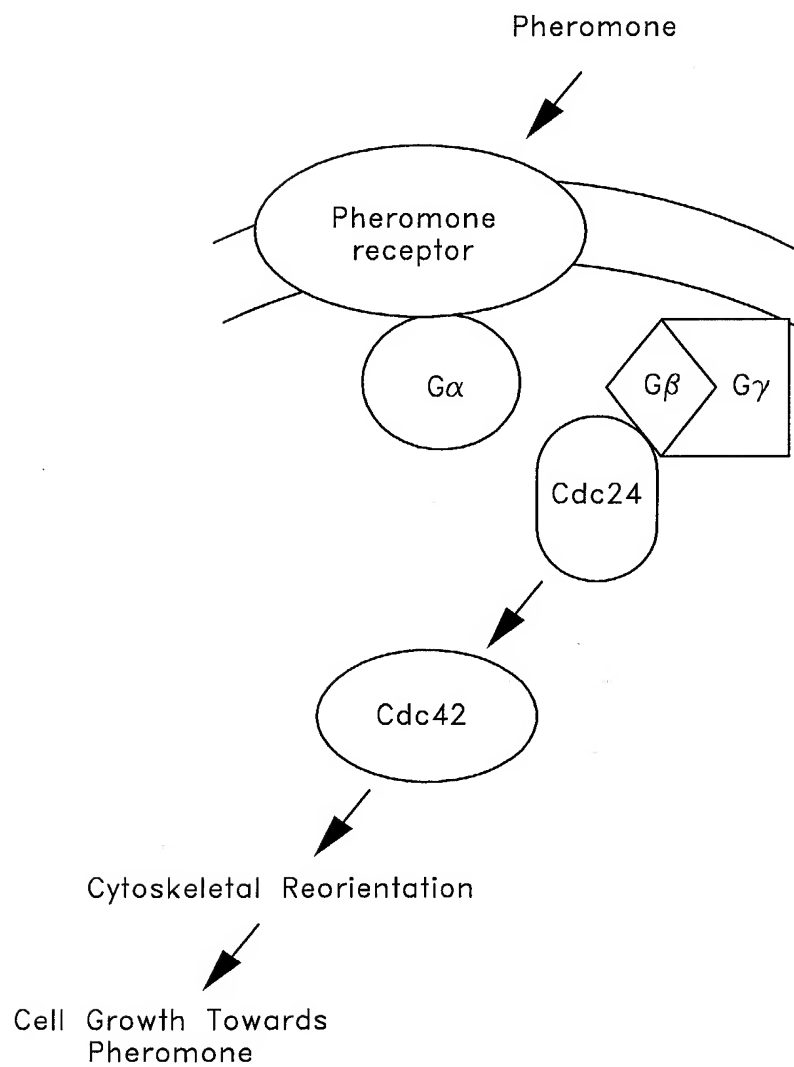


FIG. 4



● NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES ●

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FIG. 5_A

FIG. 5_B

FIG. 5



NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

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5	2113/1	ATG GAA CAT CCA CCA GCA GCT CTC AGA ACA	2143/11	TTT TCA ACC CAA TCA ACT TCA TCT TTG AAT
	M E H P P A A L R T	F S T Q S T S S L N		
10	2173/21	TCA GTA AGT ACT GTT TCG TCT TCA AGA ATT	2203/31	GTT TCT CTG GGC CCA GTC AAT ATA AAC AAT
	S V S T V S S S R I	V S S G P V N I N N		
	2233/41	TTC AAT AAA CCA AGT ACT CCC AAA GAC CAT	2263/51	TTA TTC TAT CGA TGT GAA TCA CTA AAA CGA
	F N K P S T P K D H	L F Y R C E S L K R		
15	2293/61	AAA CTA CAA AAA ATC CCT GGC ATG GAA CCA	2323/71	TTT TTG AAC CAA GCT TTC AAT CAG GCT GAA
	K L Q K I P G M E P	F L N Q A F N Q A E		
	2353/81	CAA CTC AGT GAA CAA CAA GCA TTG GCT TTG	2383/91	GCA CAG GAA AGA AGC AAT GGA AAT GGA CAT
20	Q L S E Q Q A L A L	A Q E R S N G N G H		
	2413/101	AGT AAT GGC AAA CGT CAT CAA TCA TTA GAC	2443/111	GGT GCC ATG AAT AGA CTT TCA GTT GGT TCT
	S N G K R H Q S L D	G A M N R L S V G S		
25	2473/121	GAT AGT AGT TCG ATC CAA GGT TCA TTG ACA	2503/131	CGA ATG GCC ACC AAT GCG TCA ACG TCA TCT
	D S S S I Q G S L T	R M A T N A S T S S		
	2533/141	TTA ATC AGT GGT ATG CCA AAC AAC AAC ACT	2563/151	TTA TTT ACG TTT ACT GCA GGG GTT TTA CCA
	L I S G M P N N N T	L F T F T A G V L P		
30	2593/161	GCT AAT ATT AGT GTC GAT CCT GCT ACC CAT	2623/171	CTT TGG AAA TTG TTC CAA CAA GGG GCC CCC
	A N I S V D P A T H	L W K L F Q Q G A P		
	2653/181	TTT TGT GTT CTT ATC AAT CAT ATC CTT CCT	2683/191	GAT TCC CAA ATA CCA GTT GTC AGT TCT GAT
35	F C V L I N H I L P	D S Q I P V V S S D		
	2713/201	GAC TTG AGA ATT TGC AAA AAA TCA GTA TAT	2743/211	GAC TTT TTA ATT GCC GTC AAG ACA CAA TTG
	D L R I C K K S V Y	D F L I A V K T Q L		
	2773/221	AAT TTT GAT GAC GAG AAT ATG TTC ACT ATA	2803/231	TCC AAT GTT TTC TCC GAC AAT GCC CAA GAT
40	N F D D E N M F T I	S N V F S D N A Q D		
	2833/241	TTA ATC AAG ATT ATT GAT GTC ATT AAT AAA	2863/251	CTA CTT GCT GAG TAC TCA GAT GCT AGT GAC
	L I K I I D V I N K	L L A E Y S D A S D		
45	2893/261	CTG GGT GGT GGC GAT GAA GAT GTA AAT ATG	2923/271	GAT GTT CAA ATT ACC GAT GAA AGA TCA AAA
	S G G G D E D V N M	D V Q I T D E R S K		
	2953/281	GTT TTC CGA GAA ATT ATC GAA ACA GAA AGA	2983/291	AAA TAT GTT CAA GAC TTG GAA CTA ATG TGT
50	V F R E I I E T E R	K Y V Q D L E L M C		
	3013/301	AAA TAC CGT CAA GAT CTA ATT GAA GCC GAA	3043/311	AAT TTG TCT TCA GAA CAA ATT CAC TTG TTA
	K Y R Q D L I E A E	N L S S E Q I H L L		
	3073/321	TTC CCA AAT TTA AAT GAG ATT ATT GAT TTT	3103/331	CAA AGA CGA TTC CTC AAT GGG TTA GAA TGT
55	F P N L N E I I D F	Q R R F L N G L E C		
	3133/341	AAC ATC AAT GTA CCT ATT AGA TAT CAA AGA	3163/351	ATT GGA TCA GTA TTT ATT CAT GCT TCT TTG
	N I N V P I R Y Q R	I G S V F I H A S L		
60	3193/361	GGC CCT TTC AAT GCT TAT GAA CCT TGG ACT	3223/371	ATA GGA CAA TTG ACG GCG ATT GAT TTG ATC
	G P F N A Y E P W T	I G Q L T A I D L I		
	3253/381	AAC AAA GAA GCT GCT AAT TTG AAA AAA TCG	3283/391	TCA AGT CTA CTT GAT CCT GGG TTT GAA CTT
65	N K E A A N L K K S	S S L L D P G F E L		
	3313/401	CAA TCG TAT ATA TTA AAG CCG ATC CAA AGA	3343/411	TTG TGT AAA TAC CCA CTT TTG TTG AAA GAG
	Q S Y I L K P I Q R	L C K Y P L L L K E		
	3373/421	TTA ATC AAA ACA TCA CCA GAA TAT TCA AAA	3403/431	CAG GAC CCC CAT GGC AGC TCG TCA TCG ACA
70	L I K T S P E Y S K	Q D P H G S S S S T		
	3433/441	TCA TTC AAT GAA TTA TTG GTG GCT AAA ACT	3463/451	GCA ATG AAA GAA TTG GCA AAT CAA GTC AAT
	S F N E L L V A K T	A M K E L A N Q V N		

FIG. 5A



LEOTIDE SEQUENCES AND PROTEIN SEQUENCES

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	3493/461		3523/471
	GAG GCG CAA AGA CGA GCA GAA AAT ATC GAA		CAT TTG GAA AAA CTA AAA GAA AGA GTA GGT
	E A Q R R A E N I E		H L E K L K E R V G
5	3553/481		3583/491
	AAT TGG CGT GGG TTT AAT TTG GAT GCT CAA		GGA GAA CTA TTA TTC CAC GGA CAA GTT GGG
	N W R G F N L D A Q		G E L L F H G Q V G
	3613/501		3643/511
	GTT AAA GAT GCT GAA AAT GAA AAG GAA TAC		GTT GCT TAT CTT TTT GAA AAA ATC GTA TTT
10	V K D A E N E K E Y		V A Y L F E K I V F
	3673/521		3703/531
	TTT TTC ACA GAA ATT GAT GAT ACC AAA AAA		TCT GAT AAA CAG GAA AAG AAG AGC AAG TTT
	F F T E I D D T K K		S D K Q E K K S K F
	3733/541		3763/551
15	TCG ACA AGA AAG AGA TCA ACT TCA TCA AAT		CTT AGT TCA TCG ACT ACT AAT TTG TTG GAA
	S T R K R S T S S N		L S S S T T N L L E
	3793/561		3823/571
	TCA ATA AAC AAT TCC CGA AAG GAT AAC ACA		TTG CCA TTG GAA TTA AAG GGA AGA GTT TAT
	S I N N S R K D N T		L P L E L K G R V Y
20	3853/581		3883/591
	ATA TCG GAG ATT TAT AAC ATT TCC GCA CCA		AAC ACT CCT GGC TCA ACT CTA ATC ATC TCA
	I S E I Y N I S A P		N T P G S T L I I S
	3913/601		3943/611
	TGG TCA GGT AGA AAG GAA AGC GGC TCA TTC		ACT TTG AGA TAT CGT AGT GAA GAA GCC AGA
25	W S G R K E S G S F		T L R Y R S E E A R
	3973/621		4003/631
	AAC CAA TGG GAA AAG TGT TTA CGT GAT TTG		AAG ACT AAT GAA ATG AAT AAA CAA ATT CAT
	N Q W E K C L R D L		K T N E M N K Q I H
	4033/641		4063/651
30	AAG AAG TTA CGT GAT TCC GAC CTG TCA TTT		AAT ACT GAT GAC TCT GCC ATA TAT GAT TAC
	K K L R D S D S S F		N T D D S A I Y D Y
	4093/661		4123/671
	ACG GGT ATT AGT ACG TCA CCA GTC AAT CAA		TCA ACT CAA CAA CAA TAC TAT GAT CAT CGG
	T G I S T S P V N Q		S T Q Q Q Y Y D H R
	4153/681		4183/691
35	GGC TCT CAC AGT TCC CGC CAT CAC TCA TCG		TCA TCC ACT TTG AGT ATG ATG AAG AAT AAT
	G S H S S R H H S S		S S T L S M M K N N
	4213/701		4243/711
	AGA GTT AAA TCT GGT GAT TTG AGT AGA ATA		TCT TCA ACT TCA ACA ACA TTA GAT TCT TTC
40	R V K S G D L S R I		S S T S T T L D S F
	4273/721		4303/731
	AGT AAC AAC TTG AAT GGG TCA CCA AAT ACC		ACT AAT CCA TCT TTG ATG TCT TCA GAT GCC
	S N N L N G S P N T		T N P S L M S S D A
	4333/741		4363/751
45	ACC AAA ACA ATT CCA ACA TTT GAC GTT GCA		ATT AAA TTG CTT TAC AAA TCG ACA GAA TTG
	T K T I P T F D V A		I K L L Y K S T E L
	4393/761		4423/771
	TCA GAG CCA TTG ATT GTC AAT GCA CAA ATT		GAG TAT AAT GAC CTT TTA CAG AAA ATT ATC
	S E P L I V N A Q I		E Y N D L L Q K I I
	4453/781		4483/791
50	TCC CAG ATT ATC ACT TCG AAC TTG GTG GCA		GAT GAT GTC AAT ATT AGT CGA TTG AGA TAT
	S Q I I T S N L V A		D D V N I S R L R Y
	4513/801		4543/811
	AAA GAC GAC GAA GGA GAC TTT GTG AAT TTG		AAT TCA GAT GAT GAT TGG GGG TTA GTG CTT
55	K D D E G D F V N L		N S D D D W G L V L
	4573/821		4603/831
	GAT ATG TTA ACC AGT GAA GAC TTT TAC CAA		ACA TCA AGC AAT GAA AAA CGA CTG GTG ACA
	D M L T S E D F Y Q		T S S N E K R S V T
	4633/841		
60	GTG TGG GTT TCT TGA		
	V W V S *		

FIG. 5_B



NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

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5 Blastp line up of S.c. Cdc24p and C.a. Cdc24p

S.c. Cdc24p: 1 MAIQ---TR-FA 8
M R F+
C.a. Cdc24p: 1 MEHPPAALRTFSTQ 14

10 S.c. Cdc24p: 9 SGTSLSDLKPKPSATSIIPMQNV--MNKPVTEQDSLFIHICANIRKRLEVLPLQKPFLLQ 66
S +SL+ + S+ +S N+ NKP T +D LF+ C +++++L+ +P +PFL
C.a. Cdc24p: 15 STSSLNSVSTVSSSRIVSSGPVNINNFNKPSTPKDHLFYRCESLKRKLQKIPGMEPFLLNQ 74

15 S.c. Cdc24p: 67 AYQSSEVLSEKQSLLSQKQHQELLKSNGANRDSDDLAP--TLRSSISISTATSLMSMEG 123
A+ +E LSE+Q+L L+Q++ SNG S D A ++ S S S SL M
C.a. Cdc24p: 75 AFNQAEQLSEQQALALAQERSNCGNGHSNGKRHQSLEDGAMNRLSVGSDSSSIQGSILTRMAT 134

20 S.c. Cdc24p: 124 ISYTNSNPSTATPNMEDTLLTFMSGILPITMDCDPVTQLSQLFQQGAPLCILFNSVVKPQFK 183
+ T+S S PN +TL TF+ G+LP + DP T L +LFQQGAP C+L N + P +
C.a. Cdc24p: 135 NASTSSLISGMPN-NNTLFTFTAGVLPANISVDPATHLWKLFFQQGAPFCVLINHILPDSQ 193

25 S.c. Cdc24p: 184 LPVIASDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFNSTSQLVKVLEVVELLMN 243
+PV++SDDL++CKKS+YDF++ K F+DE +FTIS+VF+++ L+K+++V+ L+
C.a. Cdc24p: 194 IPVVSDDLRIKCKSVYDFLIAVKTQLNFDENMFTISNVFSDNAQDLIKIIDVINKLLA 253

30 S.c. Cdc24p: 244 SSPTIFPSKSKTQQIMNAENQHRHQPQSSKHKNEYVKIIEKFVATERKYVVDLEILDYK 303
S + + + +E K+ +E + TERKYV DLE++ KY
C.a. Cdc24p: 254 EYSDASDSGGGDEDEV-----NMDVQITDERSKVFREIETERYVVDLELMCKY 302

35 S.c. Cdc24p: 304 RQQLDSNLITSEELYMLFPNLGDAIDFQRRFLISLEINALVEPSKQRIQALFMH-SKHF 362
RQ L+++ ++SE++++LFPNL + IDFORFL LE N V ORIG++F+H S
C.a. Cdc24p: 303 RQDLIEAENLSSEQIHLLFPNLNEIIDFQRRFLNGLECNINVPYRQIGSVFIHASLGP 362

40 S.c. Cdc24p: 363 FKLYEPWSIGQNAIEFLSSTLHKMRVDESQRFIINNKLELQSFYKPVQRLCRYPLLVK 422
F YEPW+IGQ AI+ ++ ++ S +++ ELQS++ KP+QRLC+YPLL+K
C.a. Cdc24p: 363 FNAYEPWTIGQLTAIDLINKEAANLKKSSS---LLDPGFELQSYILKPIQRLCKYPLLLK 419

45 S.c. Cdc24p: 423 ELLAE-----SSDDNNTKELEAALDISKNARSINENQRRTENHQVVKLYGRV 471
EL+ SS + EL A K +A +NE QRR EN + ++KL RV
C.a. Cdc24p: 420 ELIKTSPEYSKQDPHGSSSSTSFNELLVAKTAMKELANQVNEAQRRAENIEHLEKLKERV 479

50 S.c. Cdc24p: 472 VNWKGYRISKFGELLYFDKVFISTTSSSEPEREFEVYLFEKIILFSEVVTKSSASSLI 531
NW+G+ + GELL+ +V + +E E+E+ YLFEKI+ F+E+ K +
45 C.a. Cdc24p: 480 GNWRGFNLDAQGELLFHGQVGV---KDAENEKEYVAYLFKIVFFFTTEIDDTKSKDKQE 535

S.c. Cdc24p: 532 LKKKSSTASISASINIDNNGSPHSHYKHSNSSSSNNIHLSSSSAAAIHSSSTNSSDN 591
K K ST ++SN+ SSS ++ S NS +
C.a. Cdc24p: 536 KKSKEFSTRKRSTSSNL-----SSSTTNLLESINNSRKD 568

55 S.c. Cdc24p: 592 NSNNSSSSSLFKLSANEPKLDLRGRIMMNLNQIIPQN--NRSLNITWESIKEQGNFLLK 649
N+ L+L+GR+ I + I N +L I+W KE G+F L+
C.a. Cdc24p: 569 NT-----LPLELKGRVYISEIYNISAPNTPGSTLIISWGRKESGFTLR 613

60 S.c. Cdc24p: 650 FKNEETRDNWSSCLQQLIHDLKNEQFKARHSSSTSTSS-----TAKSSSMSPSTTT 701
+++EE R+ W CL+ L + N+Q + S S+ ++ T S+S ++ +T
C.a. Cdc24p: 614 YRSEEARNQWEKCLRDLTNEMNKQIHKKLRDSDSSFNNTDSDAIYDTGISTSPVNQSTQ 673

65 S.c. Cdc24p: 702 MNTPNHHNSRQT--HDSMASFSSSHMKRVS---DVLPKRRTTSSSFSEIKS----- 748
+H S + H S ++ S RV + TT SF + +
C.a. Cdc24p: 674 QQYYDHRGSHSSSRHSSSSTLSMMKNRVKSGDLRSISSTSTTLDSFSNNLNGSPNTTNP 733

S.c. Cdc24p: 749 --ISENFKNISIPESILFRISYNNNSNNTSSSEIFTLLVEKVNFDLIMAINSKI--SN 804
+S + +IP + ++ Y +T SE L+V ++DL+ I S+I SN
C.a. Cdc24p: 734 SLMSSDATKTIPTFDVAIKLLY---KSTELSE--PLIVNAQIEYNDLLQKIISQIITSN 787

70 S.c. Cdc24p: 805 THNNNISPIITIKIYQDEGDGFVVLGSDDEDWNVAKEMLAENNEKFLNIRLY 854
++++ I++++Y+D++GDFV L SD+DW + +ML + F +
C.a. Cdc24p: 788 LVADDVN-ISRLRYKDDEGDGFVNLNSDDDWGLVLDMLTSED--FYQTSSNEKRSVTWVVS 844

FIG. 6



NO NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

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FIG. 7A₁

FIG. 7A₂

FIG. 7A



NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

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FIG. 7A₁

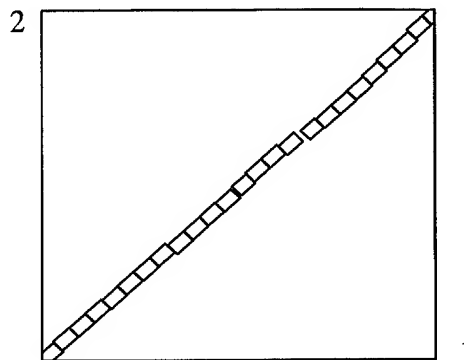
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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix 0 BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.0 wordsize: 3 Filter ☐ Align

Sequence 1 lcl|S.c. Cdc24p Length 854 (1 .. 854)

Sequence 2 lcl|C.a. Cdc24p Length 844 (1 .. 844)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 446 bits (1136), Expect = e-124
Identities = 288/881 (32%), Positives = 464/881 (51%), Gaps = 112/881 (12%)

Query: 9 SGTSLSDLKPKPSATSIIPMQNV--MNKPVTEQDSLPHICANIRKRLEVLPLQKPFLQL 66
S +SL+ + S+ +S N+ NKP T +D LF+ C +++++L+ +P ++PFL
Sbjct: 15 STSSLNSVSTVSSSRIVSSGPVNINNFNKPSTPKDHLFYRCESLKRKLQKIPGMEPFNLQ 74

Query: 67 AYQSSEVLSEKQSLLSQKQHQLLKSNGANRDSSDLAP---TLRSSSISTATSLMSMEG 123
A+ +E LSE+Q+L L+Q++ SNG S D A ++ S S S SL M
Sbjct: 75 AFNQAEQLSEQQALALAQERSNGNGHSNGKRHQSLDGAMNRLSVGSDSSSIQGSLTRMAT 134

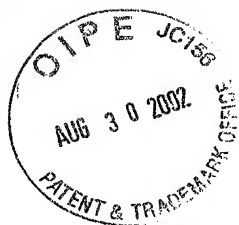
Query: 124 ISYTSNPSATPNMEDTLTFSMGILPITMDCDPVTQLSQLFQQGAPLCILFNSVKPQFK 183
+ T+S S PN +TL TF+ G+LP + DP T L +LFQQGAP C+L N + P +
Sbjct: 135 NASTSSLISGMPN--NNTLFTFTAGVLPANISVDPATHLWKLFQQGAPFCVLINHILPDSQ 193

Query: 184 LPVIASDDLKVCKKSTYDFILGCKKHFAFNDEELFTISDVFANSTSQLVKVLEVVELTMN 243
+PV++SDDL++CKKS+YDF++ K F+DE +FTIS+VF+++ L+K+++V+ L+
Sbjct: 194 IPVVSDDLRIKCKSVYDFLIYVKTQLNFDENMFITISNVFSDNAQDLIKIIDVINKLLA 253

Query: 244 SSPTIFPSKSKTQQIMNAENQHRHQPQSSKKHNEYVKIIKEFVATERKYVHDLEILDY 303
S + + + +E K+ +E + TERKYV DLE++ KY
Sbjct: 254 EYSDASDSGGGEDV-----NMDVQITDERSKVFREIIETERKYVQDLELMCKY 302

Query: 304 RQQLLDNLITSEELYMLFPNLGDAIDFQRRFLISLEINALVEPSKQRIQALFMH-SKHF 362
RQ L+++ ++SE++++LFPNL + IDFQRRFL LE N V QRIQ++F+H S
Sbjct: 303 RQDLIEAENLSSEQIHLLFPNLNEIIDFQRRFLNGLECNINVPRIYQRIQSVFIHASLGP 362

Query: 363 FKLYEPWSIGQNAIEFLSSTLHKMRVDESQRFIINNKLELQSFYKPVQRLCRYPLLK 422
F YEPW+IGQ AI+ ++ ++ S +++ ELQS++ KP+QRLC+YPLL+K
Sbjct: 363 FNAYEPWTIGQLTAIDLINKEAANLKKSSS---LLDPGFELQSYILKPIQRLCKYPLLLK 419



NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

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Query: 551 --NGSPHHSYHKRHSNSSSSNNIHL-----SSSAAAIHSSTNSSDNNNSNNSSSS 599
G P H + S + + S + I S + + N N SSS
Sbjct: 477 FWRGDPQHESFILKLRNEESHKLWMSVLNRLLLWKNEHGSPKDIRSAASTPANPVYNRSS 536

Query: 600 SLFKLSANEPKLD-LRGRIMIMNLN---QIIPQNNRSLNITWESIKEQGNFLLKFKN EET 655
K N D LR + N+N I +++S T + K+ K+ T
Sbjct: 537 QTSK-GYNSSDYDLLRTHSLDENVNSPTSISSPSSKSSPFTKTTSKDT-----KSATT 588

Query: 656 RDNWSSCLQQLIHLKNEQFKARHHSSTST-----TSSTAKSSSSMMSPTTTMNT--PNHH 708
D S +L + R +TST +SSTA S +S + +N+ +++
Sbjct: 589 TDERPSDFIRLNSEESVGTSSLRTSQTSTIVSNDSSSTASIPSQISRISQVNSLLNDYN 648

Query: 709 NSRQTH-----DSMASF---SSSHMKRVSD-----VLPKRRTTSSSFES 745
+RQ+H S++ F SSS +++ D + P++ + S+ +S+
Sbjct: 649 YNRQSHITRVYSGTDDGSSVSIFEDTSSSTKQKIFDQPTTNDCDVMRPRQYSYSAGMKSD 708

Query: 746 IKSISENFKNSIPESSILFRISYNNNSNNTSSSEI----FTLLVEKVWNFDDLIMAINSK 801
+ S+ SS +S N +N + L+V FD+L+ + K
Sbjct: 709 GSLLPSTKHTSLSSSSTSTSLSVRNTTNVKIRLRLHEVSLVLVVAHDITFDELLAKVEHK 768

Query: 802 IS--NTHNNNISPI TKIKYQDEDDGDFVVLGSDDEDWNVAKE 839
I + ++KY DEDGDF+ + SDED +A E
Sbjct: 769 IKLCGILKQAVPFRVRLKYVDEDDGDFITITSDEDDVLMFAFE 808

CPU time: 0.26 user secs. 0.04 sys. secs 0.30 total secs.

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 10384

Number of Sequences: 0

Number of extensions: 671

Number of successful extensions: 13

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 834

length of database: 90,077,593

effective HSP length: 61

effective length of query: 773

effective length of database: 83489227

effective search space: 64537172471

effective search space used: 64537172471

T: 9

A: 40

X1: 16 (7.3 bits)

X2: 128 (49.9 bits)

X3: 128 (49.9 bits)

S1: 41 (21.7 bits)

S2: 73 (32.8 bits)

FIG. 7A₂



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FIG. 7B₁

FIG. 7B₂

FIG. 7B



NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

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FIG. 7B₁

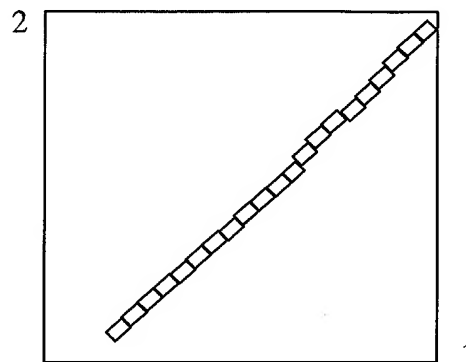
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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☐ Align

Sequence 1 lcl|S.c. Cdc24p Length 854 (1..854)

Sequence 2 lcl|S.p. Cdc24p Length 834 (1..834)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 238 bits (601), Expect = 1e-61
Identities = 212/760 (27%), Positives = 348/760 (44%), Gaps = 94/760 (12%)

```
Query: 156 DPVTQLSQLFQQGAPLCILFNSVKPQFKLFVIASDDLK---VCKKSIYDFILGCKKHFAF 212
          + G PLC LFN + + KL V +S L+ VCK S+Y F+L CK
Sbjct: 67 DPVTEIWLFCRLGYPLCALFNCLPVKQKLEVNSSVSLENTNVCKASLYRFMLMCKNELGL 126

Query: 213 NDEELFTISDVFANSTSQLVKVLEVETLMNSSPTIFPSKSKTQQIMNAENQHRHQPPQS 272
          D LF+IS+++ ST+ LV+ L+ +E L+ +KS + + ++ S
Sbjct: 127 TDAALFSISEIYKPSTAPLVRALQTIELLLKKYEVSN+TKSSSTPSPSTDDNVPTGTILNS 186

Query: 273 SKKHNEYVKIIKEFVATERKYVHDLILDKYRQQLDLSNLTSEELYMLFPNLGDAIDFQ 332
          ++ E TE KY+ DLE L Y L +++ + + +F NL + +DFQ
Sbjct: 187 LIASGR--RVTAELYETELKYIQDLEYLSNYMVILQQKQILSQDTILSIFTNLNEILDFO 244

Query: 333 RRFLISLEINALVEPSKQRIGALFMHSHKHFPLYEPWSIG-QNAAIEFLSSTLHKMRVDE 391
          RRFL+ LE+N + +QR+GALF+ + F +Y+ + NA + + ++V
Sbjct: 245 RRFLVGLMNLSLPVEEQRLGALFIALEEGFSVYQVFCTNFPNAQQLIIDNQNLKLVAN 304

Query: 392 SQRFIINKLELQSFYLYKPVQRLCRYPLLVKELL-AESSDDNNTKELEAALDISKNIARS 450
          ++ EL + L KP+QR+C+YPLL+ +LL S +EL+ + +A
Sbjct: 305 ----LLEPSYELPALLIKPIQRICKYPLLLNQLLKGTSPSGYQYEEELKQGMACVVRVANQ 360

Query: 451 INENQRRRTENHQVVKLYGRVNVWKGYSRISKFGELLYFDKVFISTNSSSEPEREFEVYL 510
          +NE +R EN + +L RV++WKGY + FG+LL +D V + ++ ERE+ VYL
Sbjct: 361 VNETRRIHENRNAIIELEQRVIDWKGYSLQYFGQLLVWDVVNV----CKADIERYHYVYL 416

Query: 511 FEKIIILFSEVVT-KKSASSLILKKKSSTSAS-----ISASNITDN----- 550
          FEKI++ E+ T K+ A S+ + KK+ S I SNIT
Sbjct: 417 FEKILLCKEMSTLKRQARSISMNKKTKRLDSLQKGRILTSNITTVPNHHMGSYAIQI 476
```



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FIG. 7B₂

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```
Query: 423 ELLAE-----SSDDNNTKELEAALDISKNIARSINENQRRRTENHQVVKKLYGRV 471
      EL+          SS + EL A K +A +NE QRR EN + ++KL RV
Sbjct: 420 ELIKTSPEYSKQDPHGSSSSSTSFNELLVAKTAMKELANQVNEAQRRAENIEHLEKLKERV 479

Query: 472 VNWKGYRISKFGELLYFDKVFISTTSSSEPEREFVYLFEKIIILFSEVVTKKSASSLI 531
      NW+G+ + GELL+ +V + +E E+E+ YLFEKI+ F+E+ K +
Sbjct: 480 GNWRGPNLDAQGELLFHGQVGV----KDAENEKEYVAYLFEKIVFFFTTEIDDTKKSDKQE 535

Query: 532 LKKKSSTASISASNITDNNGSPHSHYKRRHSNSSSSNNIHLSSSSAAAIHSSSTNSSDN 591
      K K ST ++SN+ SSS ++ S NS +
Sbjct: 536 KKSFKSTRKRSTSSNL-----SSSTTNLLESINNSRKD 568

Query: 592 NSNNSSSSSLFKLSANEPKLDLRGRIMIMNLNQIIPQN--NRSLNITWESIKEQGNFLK 649
      N+ L+L+GR+ I + I N +L I+W KE G+F L+
Sbjct: 569 NT-----LPLELKGRVYISEIYNISAPNTPGSTLIISWSGRKESGSPFLR 613

Query: 650 FKNEETRDWSSCLQQLIHDLDKNEQFKARHHSSTSTSS-----TAKSSSMMSPTTT 701
      +++EE R+ W CL+ L + N+Q + S S+ ++ T S+S ++ +T
Sbjct: 614 YRSEEARNQWEKCLRDLDKTNEMNKQIHKLRDSDSSFNTPDSDAIYDYGISTSPVNQSTQ 673

Query: 702 MNTPNHHNSRQT--HDSMASFSSSHMKRVS----DVLPKRRTTSSSFSESIKS----- 748
      +H S + H S ++ S RV + TT SF + +
Sbjct: 674 QQYYDHRGSHSSRHSSSSSTLSMMKNNRVKSGDLRSISSTSTLDSFSNNLNGSPNTTNP 733

Query: 749 --ISENFKNSIPESSILFRISYNNNSNNTSSSEIFTLLVEKVWNFDDLIMAINSKI--SN 804
      +S + +IP + ++ Y +T SE L+V ++DL+ I S+I SN
Sbjct: 734 SLMSSDATKTIPTFDVAIKLLY----KSTELSE--PLIVNAQIEYNDLLQKIISQIITSN 787

Query: 805 THNNNISPIITKIKYQDEDDGDFVVLGSDDEDWNVAKEMLAENN 845
      ++++ I++++Y+D++GDFV L SD+DW + +ML +
Sbjct: 788 LVADDVN-ISRLRYKDDEGDFVNLNSDDDDWGLVLDMLTSED 827
```

CPU time: 0.26 user secs. 0.02 sys. secs 0.28 total secs.

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 12253

Number of Sequences: 0

Number of extensions: 709

Number of successful extensions: 15

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 844

length of database: 90,077,593

effective HSP length: 63

effective length of query: 781

effective length of database: 83353792

effective search space: 65099311552

effective search space used: 65099311552

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 128 (49.9 bits)

X3: 128 (49.9 bits)

S1: 42 (21.9 bits)

S2: 73 (32.8 bits)



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Sc KLPVIASDDLKVCCKKSIYDFIL (SEQ ID No 25)

++PV++SDDL++CKKS+YDF++

Ca QIPVVSSDDLRLCKKSVYDFLI (SEQ ID No 26)

Sc = *Saccharomyces cerevisiae*

Ca = *Candida albicans*

FIG. 8



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FIG. 9A Fungal Cdc24's

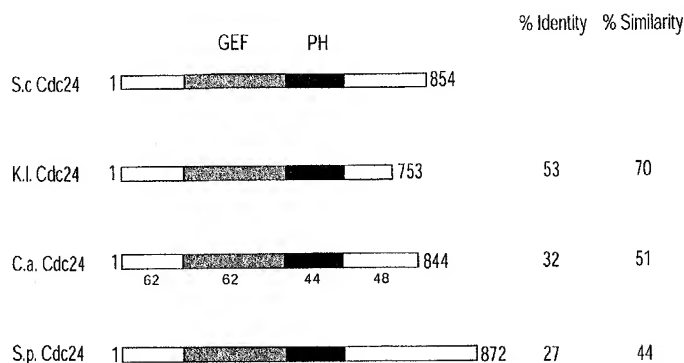


FIG. 9B

Guanine nucleotide exchange factor domain of CaCDC24 is homologous to other fungal Cdc24p's

```

S.c. 227 STSQLVLELVVETLMNSSPTIFPSKSKTQIMNAENQRRHQPQSSSKHNHYVKIIEKF
K.l. 221 STDHFLKVLVDVNTLLNAAPEVFPQIDMSTOLE-----S-ORLAKPQTEYDKIVKEF
C.a. 237 NAQDLIKITIDVINKLLAEVSDASDGGGDEDVN-----MDVQITDERSKVFREI
S.p. 179 STAPLVRALQTIETLLKKYEVSNNTTKSSSTPSPSTDDN--VPTGTENSLIASGRRTAEL

S.c. 287 VATERKIVHOLEHFDKRYRQQLDSNLTSEELTYLFPNIDQADDFQRRLYSUBINALVE
K.l. 272 IETERRKYHOLEVFNKRYRQQLDSNLTSEELTYLFPNIDQADDFQRRLYSUBINALVE
C.a. 286 IETERRKYHOLEVFNKRYRQQLDSNLTSEELTYLFPNIDQADDFQRRLYSUBINALVE
S.p. 237 YETERRKYHOLEVFNKRYRQQLDSNLTSEELTYLFPNIDQADDFQRRLYSUBINALVE

S.c. 347 PSKQRIQALPMSKH-EPKLYEPWSIGQAAATPFLSTLHKRVVDESGRPIINNELILOS
K.l. 332 SKQRIQALPMSKH-EPKLYEPWSIGQAAATPFLSTLHKRVVDESGRPIINNELILOS
C.a. 346 IYQRIQGVTEASLOPNAVEPWTIGQTALDINKEAANLKSST--LDPGFELLOS
S.p. 297 VEBQRIQALPMSKH-EPKLYEPWSIGQAAATPFLSTLHKRVVDESGRPIINNELILOS

S.c. 406 PLKPPVORLCYPLLLKELHQAEGD-----SKELEIALQAKSIARNINEN
K.l. 390 PLKPPVORLCYPLLLKELHQAEGD-----SKELEIALQAKSIARNINEN
C.a. 403 YLKKPPORLCYPLLLKELHQAEGD-----SKELEIALQAKSIARNINEN
S.p. 353 LKPPVORLCYPLLLKELHQAEGD-----SKELEIALQAKSIARNINEN

S.c. 455 QRRTENHGVVKKLYGRVNNKGYRIKPGELLYFDVPISTNNSGEPERSEVYLFEKI
K.l. 437 QRRTENHGVVKKLYGRVNNKGYRIKPGELLYFDVPISTNNSGEPERSEVYLFEKI
C.a. 463 QRRTENHGVVKKLYGRVNNKGYRIKPGELLYFDVPISTNNSGEPERSEVYLFEKI
S.p. 403 QRRTENHGVVKKLYGRVNNKGYRIKPGELLYFDVPISTNNSGEPERSEVYLFEKI

```

FIG. 9C

Homology of Ste4p binding region

```

S.c. 170 PLCILFNSVKPQFKLPVLASDDLK---VCKKSIYDFILGCKKHFAFNDEELFTISDVFN
K.l. 164 PLCILFNAVRPQSKLTIVSSDDLK---ICKKSIYDFILGCKKHFAFNDEELFTISDVFN
C.a. 180 PLCVILNHILPDSQIFVSSDDLK---ICKKSIYDFILGCKKHFAFNDEELFTISDVFN
S.p. 119 PLCALFNCILPVKQKLEVNSSVSENTNVCKASLYRFMLCKNELGLTDAALFSISSEIYKP

S.c. 227 STSQLVLELVVETLMNSSPTIFPSKSKTQIMNAENQRRHQPQSSSKHNHYVKIIEKF
K.l. 221 STDHFLKVLVDVNTLLNAAPEVFPQIDMSTOLE-----S-ORLAKPQTEYDKIVKEF
C.a. 237 NAQDLIKITIDVINKLLAEVSDASDGGGDEDVN-----MDVQITDERSKVFREI
S.p. 179 STAPLVRALQTIETLLKKYEVSNNTTKSSSTPSPSTDDN--VPTGTENSLIASGRRTAEL

```

FIG. 9D

Homology of Bem1p binding region

```

S.c. 774 -----NTSSSEIFLLVEKVVNFDDLIMAINSKISNTHNNNI-S-PTIKIKYQD
K.l. 789 -----DFYTVLVSLDCSAEDLLAIAKRKLAHLG-----VITKVKYQD
C.a. 746 TFD--VAIKLLYKSTELSEPIIVNAQIEYNDLLQKHISQIITSNLVADDV-NISRLRYKD
S.p. 768 SVRNTTNVKTIRLRLEHVSLEVVVAHDITFDELLAKVEHKIKLCITLKQAVPFVRVRLKYVD

S.c. 822 EDGDFVVLGSDDEDWNVAKEMLA-----ENNEKFLNIRLY--
K.l. 723 EDGDFVMLESDDDWVYVVKDMLK-----ESNERLLNVW----
C.a. 804 EDGDFVNLNSDDDDWGLVLDMLTSEDFYQTSSEKRSVTVVVS--
S.p. 828 EDGDFITITISDEDVLMFAFETCFELMDPVHNKGMDTVSLHVVVYF

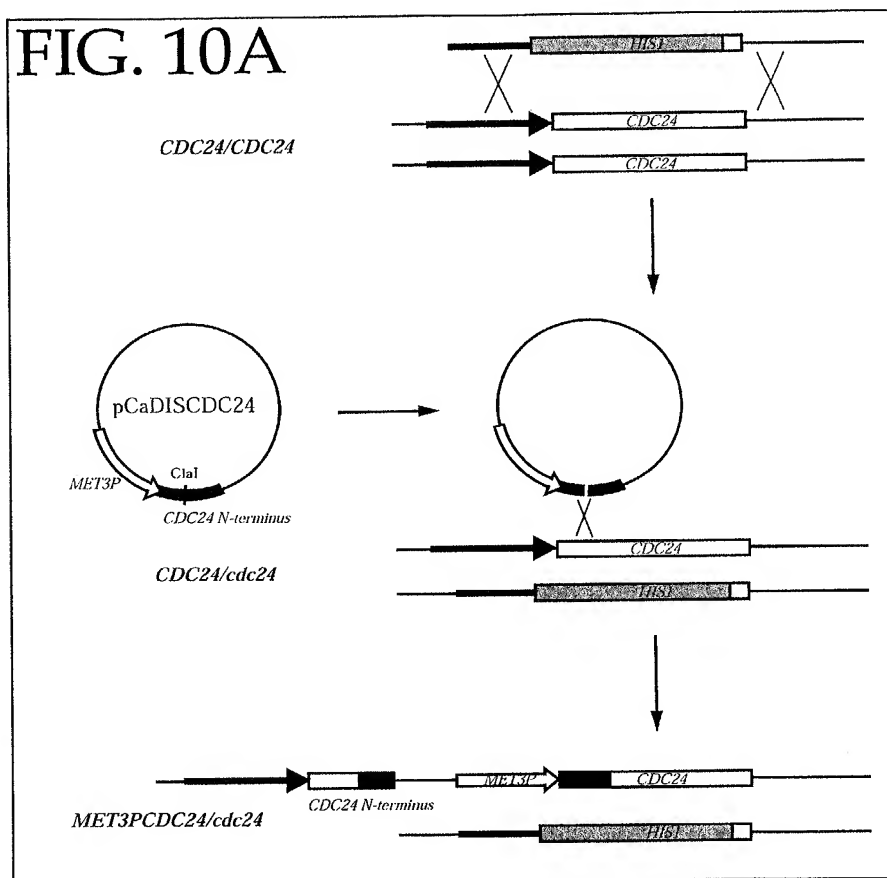
```




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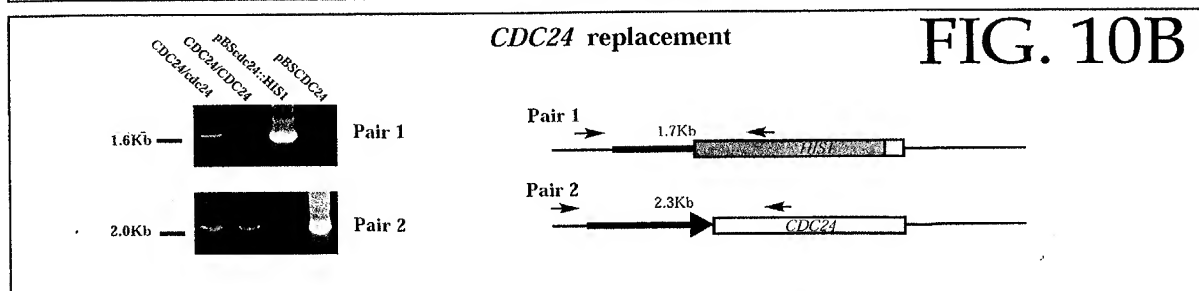
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FIG. 10A



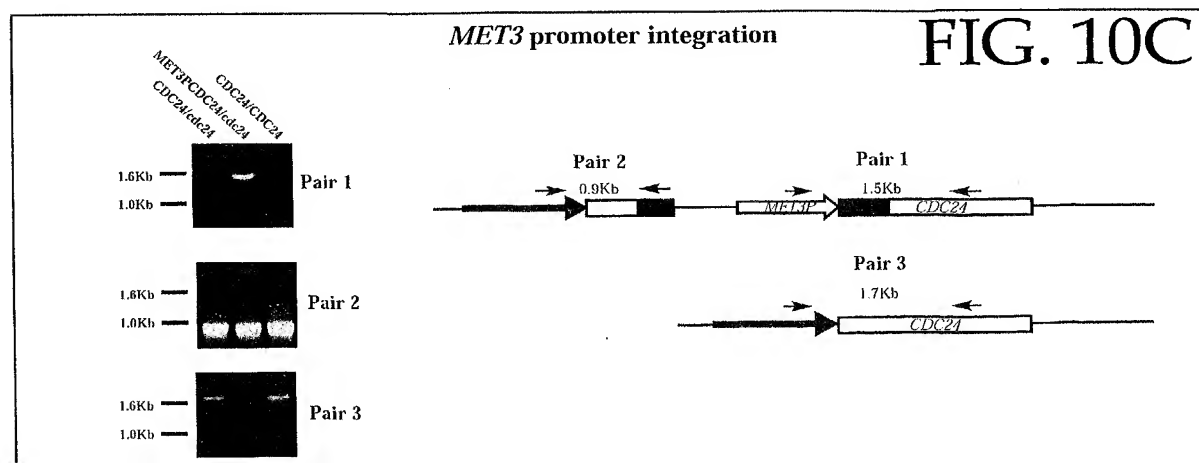
CDC24 replacement

FIG. 10B



MET3 promoter integration

FIG. 10C





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FIG. 11A

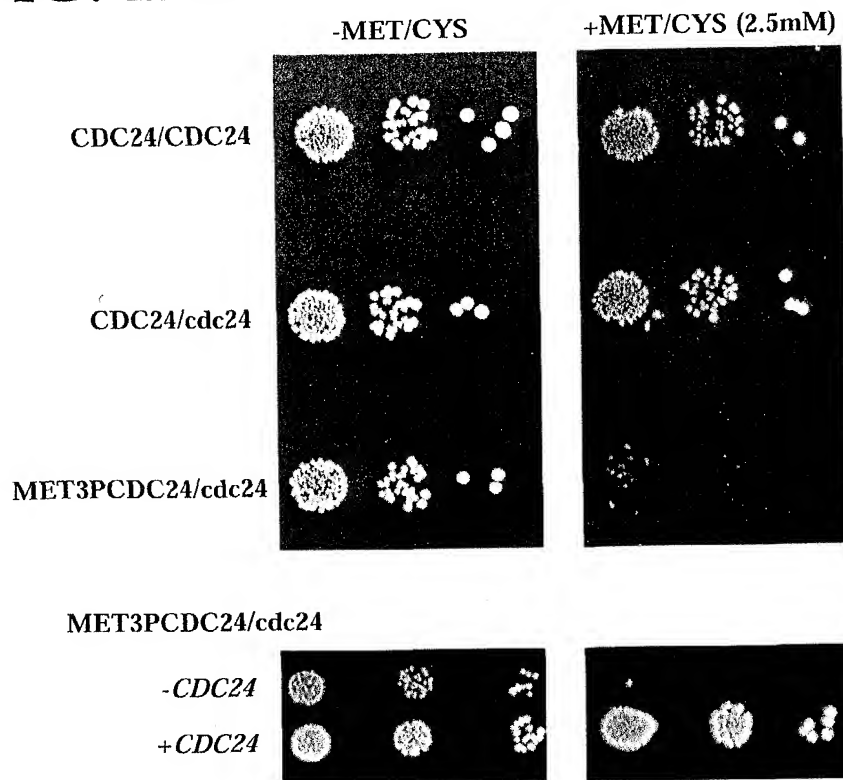
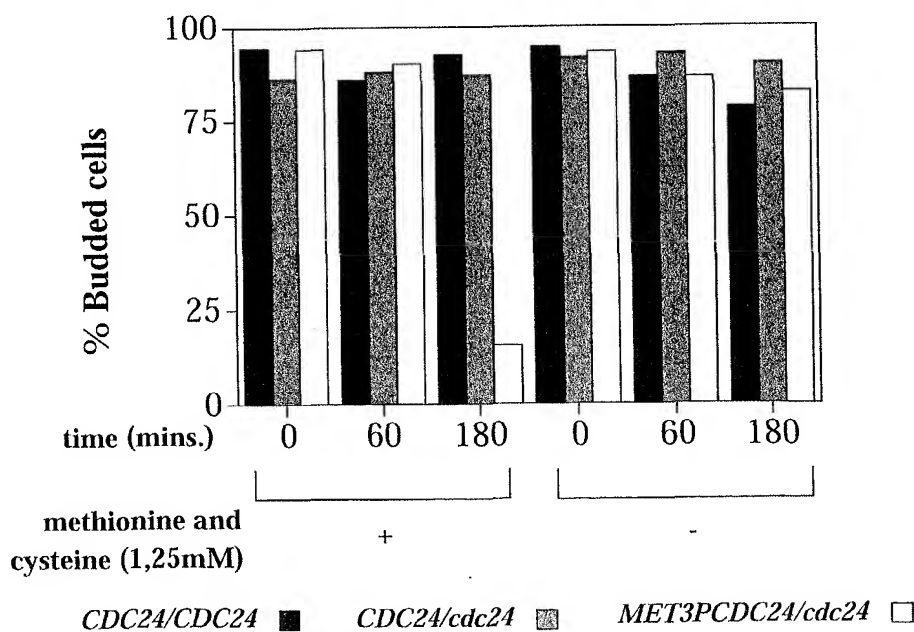


FIG. 11B



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FIG. 12A

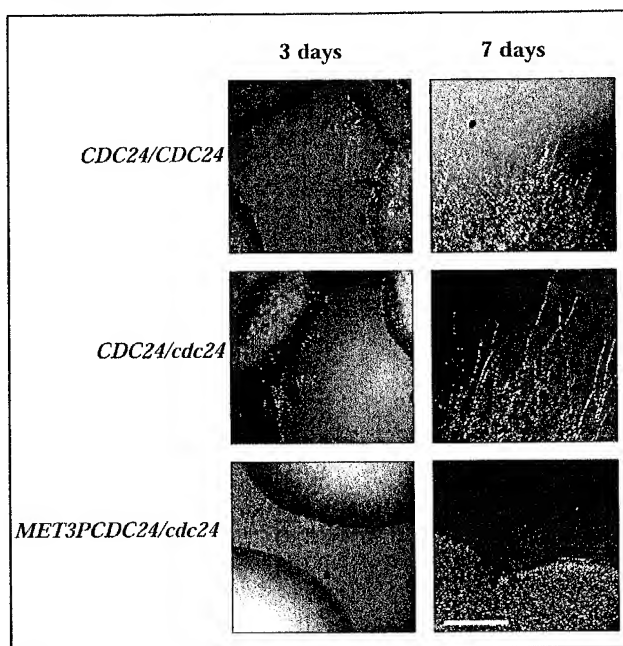


FIG. 12B

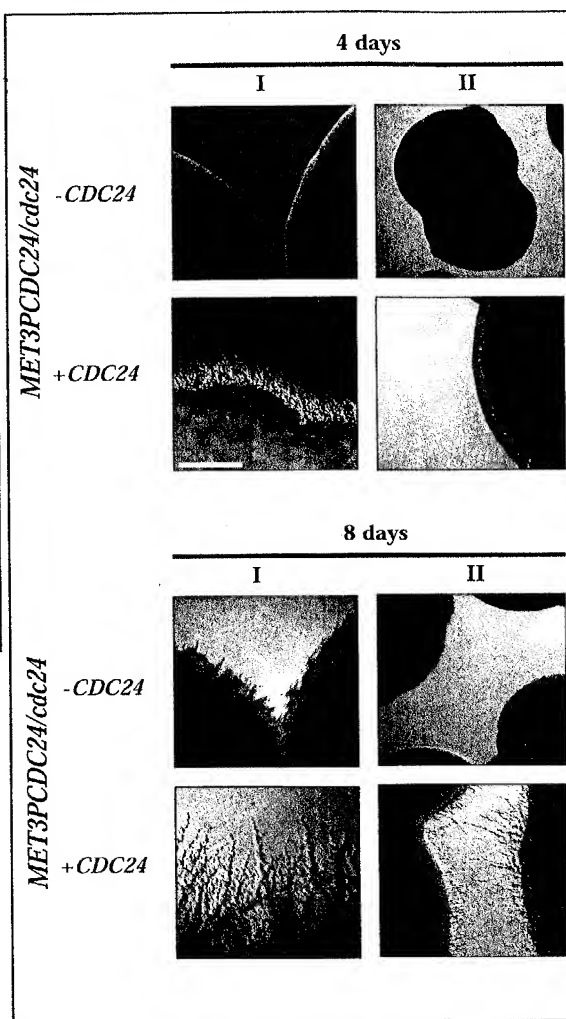
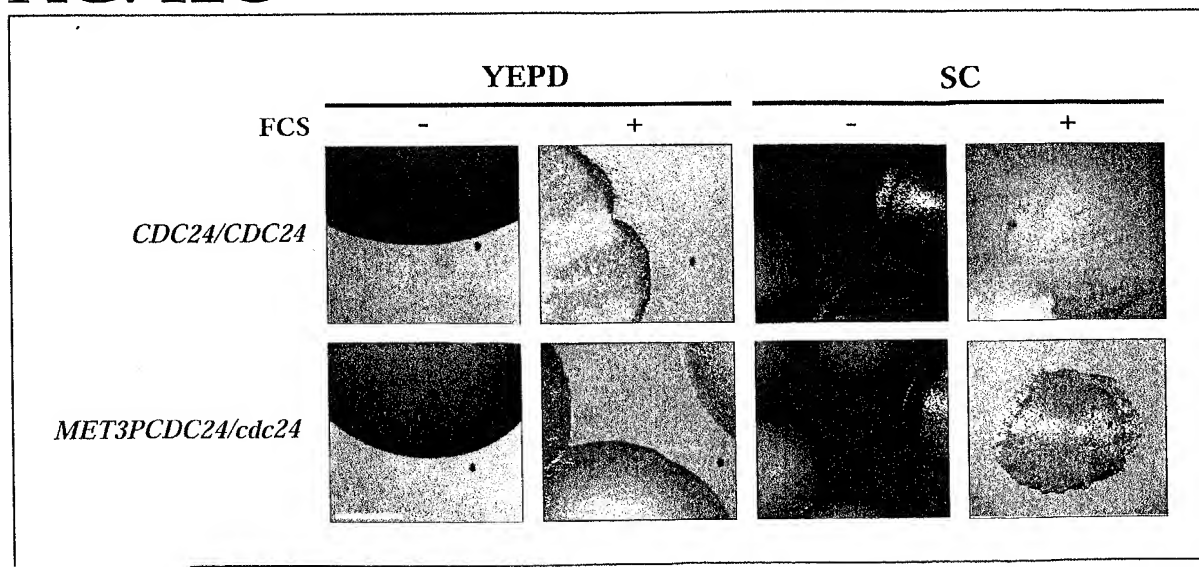


FIG. 12C





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FIG. 14A

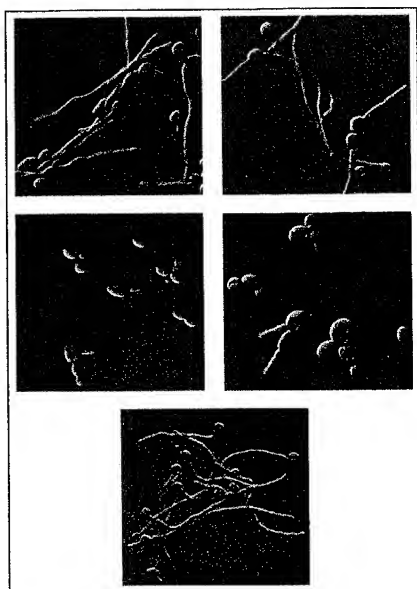


FIG. 14B

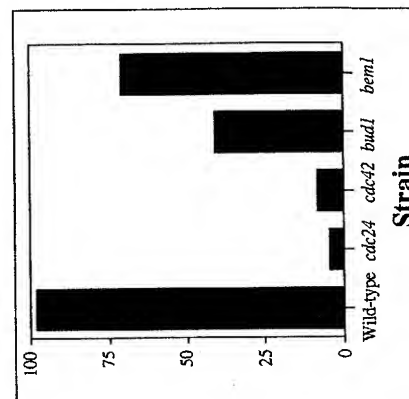


FIG. 13A

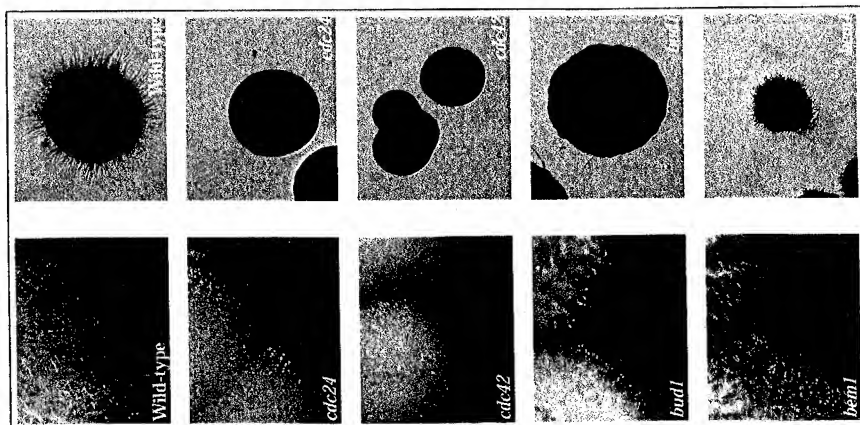


FIG. 13B





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FIG. 15A

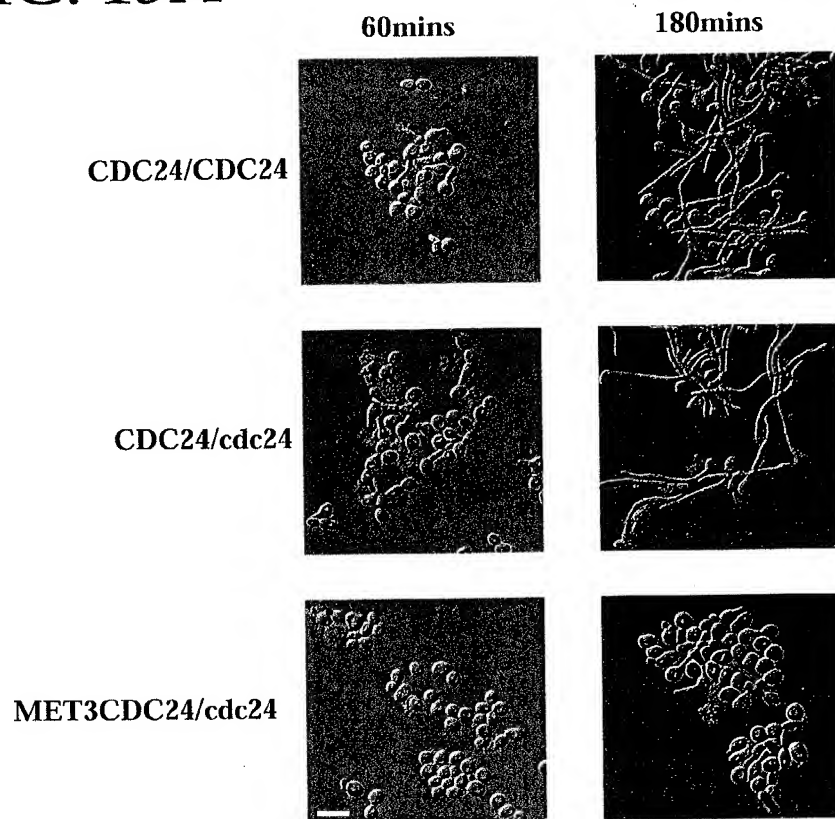
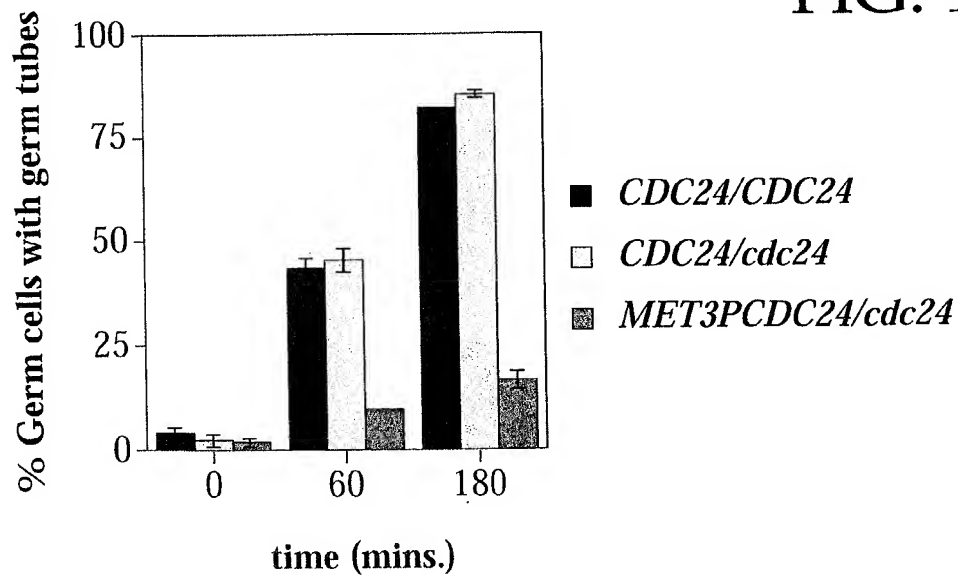


FIG. 15B



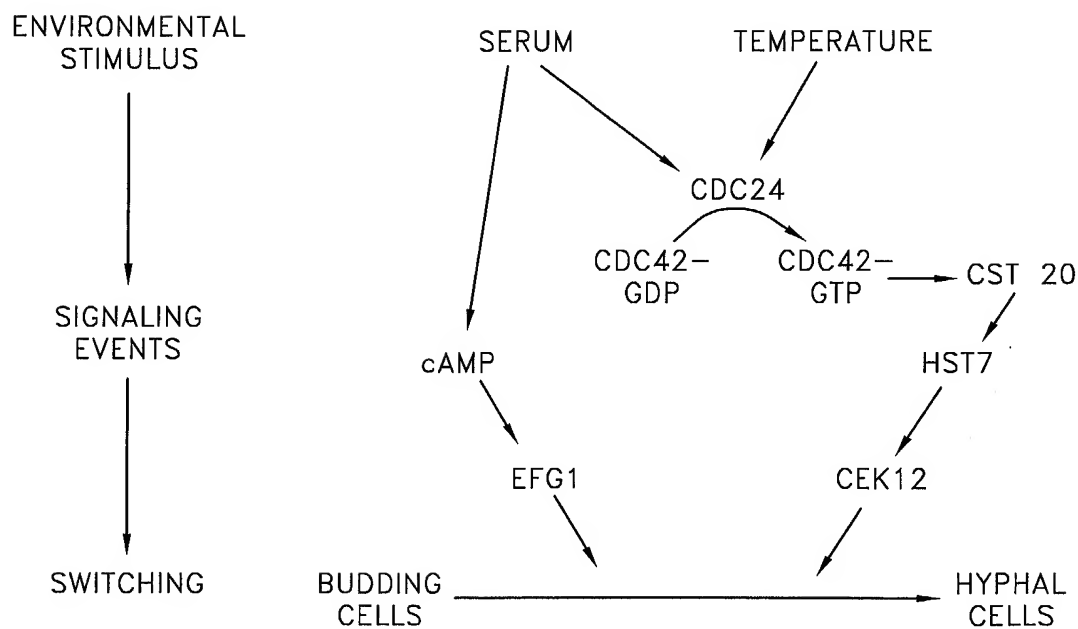


FIG. 16



NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

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FIG. 17_A

FIG. 17_B

FIG. 17_C

FIG. 17_D

FIG. 17_E

FIG. 17



NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

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A. *cdc24* (wt)

5

SEQ. I.D. NO:1

DNA:

ccccctctgtatacttttcaactctgtgaagccgcaatttaaattaccggtaatagcatctgacgatttgaaagtctgtaaaaatccatttatgactt
10 tatattgggctgcaagaaacactttgcatttaacgatgaggagcttttactatatccgacgttttgccaactcgacgtcccagctgggtcaaagt
gctagaagtagtagaaacgctaataatgaattccagc

SEQ. I.D. NO:2

Protein:

15 PLCILFNSVKPQFKLPVIASDDLKVCCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ
LVKVLEVVELTMNSS

B. *cdc24-m1*

20 SEQ. I.D. NO:3

DNA:

ccccctctgtatacttttcaactctgtgaagccgcaatttaaattaccggtaatagcatttgacgatttgaaagtctgtaaaaatccatttatgacttt
atattgggctgcaagaaacactttgcatttaacgatgaggagcttttactatatccgacgttttgccaactcgacgtcccagctgggtcaaagt
gctagaagtagtagaaacgctaataatgaattccagc

25

SEQ. I.D. NO:4

Protein:

PLCILFNSVKPQFKLPVIAFDDLKVCCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ
LVKVLEVVELTMNSS

30

FIG. 17_A



FIG. 17_B

C. *cdc24-m2*

5 SEQ. I.D. NO:5

DNA:

ccccctctgtatactttcaactctgtgaagccgcaatttaaattaccggaatagcatctggcgatttgaaagtctgtaaaaatccatttatgactt
tatattgggctgcaagaaacactttgcatttaacgatgaggagctttcactatatccgacgttttgccaactcgacgtcccagctgggtcaaagt
gctagaagtagtagaaacgctaataatgaattccagc

10

SEQ. I.D. NO:6

Protein:

PLCILFNSVKPQFKLPVIASGDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ
LVKVLEV VETLMNSS

15

D. *cdc24-m3*

SEQ. I.D. NO:7

DNA:

20 cccctctgtatactttcaactctgtgaagccgcaatttaaattaccggaatagcacctgacgatttgaaagtctgtaaaaatccatttatgactt
tatattgggctgcaagaaacactttgcatttaacgatgaggagctttcactatatccgacgttttgccaactcgacgtcccagctgggtcaaagt
gctagaagtagtagaaacgctaataatgaattccagc

SEQ. I.D. NO:8

25 Protein:

PLCILFNSVKPQFKLPVIAPDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ
LVKVLEV VETLMNSS



FIG. 17c

SEQ ID NO. 10

STE4 DNA sequence (wild-type)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCAACAGTATATACAACCACAAAGTCTACAGGA
TATCTCTGCAGTGGAGGAAGAAATTCAAATAAAATAGAGGCCGCCAGACAAGAGAGTAAACAGCTTCATGCTCAAATAA
ATAAAGCAAAACACAAGATACAAGATGCAAGCTTATTCCAGATGGCCAACAAAGTTACTTCGTTGACCAAAAATAAGATC
5 AACTTAAAGCCAAATATCGTGTTGAAAGGCCATAATAATAAAATCTCAGATTTTCGGTGGAGTCGAGATTCAAACGTAT
TTTGAGTGCAAGTCAAGATGGCTTTATGCTTATATGGGACAGTGCTTCAGGTTTAAACAGAACGCTATTCCATTAGATT
CTCAATGGGTTCTTTCTGCGCTATTTGCGCATCGAGTACTTTGGTAGCAAGCGCAGGATTAAACAATAACTGTACCATT
TATAGAGTTTCGAAAGAAAACAGAGTAGCGCAAAACGTTGCGTCAATTTTCAAAGGACATACTTGCTATATTTCTGACAT
TGAATTTACAGATAACGCACATATATTGACAGCAAGTGGGGATATGACATGTGCCTTGTGGGATATACCGAAAGCAAAGA
10 GGGTGAGAGAATATTCTGACCATTTAGGTGATGTTTTGGCATTAGCTATTCTGAAGAGCCAAACTTAGAAAATTCTTCG
AACACATTTCGCTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCCGTCCGCTGTACAAAGCTTTTA
CGTTAACGATAGTGATATTAATGCACTTCGTTTTTTCAAAGACGGGATGTGCGATTGTTGCAGGAAGTGACAATGGTGCGA
TAAATATGTATGATTTAAGGTCGGACTGTTCTATTGCTACTTTTTCTCTTTTTTCGAGGTTATGAAGAACGTACCCCTACC
CCTACTTATATGGCAGCTAACATGGAGTACAATACCGCGCAATCGCCACAAACTTTAAATCAACAAGCTCAAGCTATCT
15 AGACAACCAAGGCGTTGTTTTCTTTAGATTTTAGTGATCTGGAAGATTGATGTACTCATGCTATACAGACATTGGTTGTG
TTGTGTGGGATGTATTAAGGAGAGATTGTTGGAAAATTAGAAGGTCATGGTGGCAGAGTCACTGGTGTGCGCTCGAGT
CCAGATGGGTTAGCTGTATGTACAGGTTTCATGGGACTCAACCATGAAAATATGGTCTCCAGGTTATCAATAG

20 SEQ ID NO. 11

Ste4 Protein sequence (wild-type)

MAHQMDSITYSNNVTQQYIQPQSLQDISAVEEEIIONKIEAARQESKQLHAQINKAKHKIQDASLFQMANKVTSITKNKIN
LKPNIVLKGHNKISDFRWSRDSKRILSASQDGFMLIWDSASGLKQNAIPLDSQWVLSCAISPSSTLVASAGLNNNCTIY
25 RVSKENRVAQNVAIFKGHTCYISDIEFTDNAHILTASGDMTCALWDIPKAKRVREYSDDLGLDLALAIPEEPNLENSN
TFASCGSDGYTYIWDSRSPSAVQSFYVNDSDINALRFFKDGMSIVAGSDNGAINMYDLRSDCSIATFSLFRGYEERTPTP
TYMAANMEYNTAQSPQTLKSTSSSYLDNQGAVSLDFSASGRMLMSCYTDIGCVVWDVLKGEIVGKLEGHGGRVTGVRSSP
DGLAVCTGSWDSTMKIWSPGYQ

30

SEQ ID NO. 12

ste4-o15 DNA sequence (mutant)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCAACAGTATATACAACCACAAAGTCTACAGGA
35 TATCTCTGCAGTGGAGGAAGAAATTCAAATAAAATAGAGGCCGCCAGACAAGAGAGTAAACAGCTTCATGCTCAAATAA
ATAAAGCAAAACACAAGATACAAGATGCAAGCTTATTCCAGATGGCCAACAAAGTTACTTCGTTGACCAAAAATAAGATC
AACTTAAAGCCAAATATCGTGTTGAAAGGCCATAATAATAAAATCTCAGATTTTCGGTGGAGTCGAGATTCAAACGTAT



FIG. 17_D

TTTGAGTGCAAGTCAAGATGGCTTTATGCTTATATGGGACAGTGCTTCAGGTTTAAACAGAACGCTATTCCATTAGATT
CTCAATGGGTTCTTTCTGCGCTATTTTCGCCATCGAGTACTTTGGTAGCAAGCGCAGGATTAAACAATAACTGTACCATT
TATAGAGTTTTCGAAAGAAAACAGAGTAGCGCAAAACGTTGCGTCAATTTTCAAAGGACATACTTGCTATATTTCTGACAT
TGAATTTACAGATAACGCACATATATTGACAGCAAGTGGGGATATGACATGTGCCTTGTGGGATATACCGAAAGCAAAGA
5 GGGTGAGAGAATATTCTGACCATTTAGGTGATGTTTTGGCATTAGCTATTCCTGAAGAGCCAAACTTAGAAAATTCCTCG
AACACATTTCGCTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCCGTCGCTGTACAAAGCTTTTA
CGTTAACGATAGTGATATTAATGCACTTCGTTTTTTCAAAGACGGGATGTCGATTGTTGCAGGAAGTGACAATGGTGCGA
TAAATATGTATGATTTAAGTTCGGACTGTTCTATTGCTACTTTTTCTCTTTTTTCGAGGTTATGAAGAAGCTACCCCTACC
CCTACTTATATGGCAGCTAACATGGAGTACAATACCGCGCAATCGCCACAACTTTAAATCAACAAGCTCAAGCTATCT
10 AGACAACCAAGGCGTTGTTTCTTTAGATTTTAGTGATCTGGAAGATTGATGTACTCATGTATACAGACATTGGTTGTG
TTGTGTGGGATGTATTAAGGAGAGATTGTGGAAAATTAGAAGTCATGGTGGCAGAGTCACTGGTGTGCGCTCGAGT
CCAGATGGGTTAGCTGTATGTACAGGTTTCATGGGACTCAACCATGAAAATATGGTCTCCAGGTTATCAATAG

SEQ ID NO. 13

15 Ste4-o15 Protein sequence (mutant)

MAHQMDSITYSNNVTQQYIQPQSLQDISAVEEEIQNKIEAARQESKQLHAQINKAKHKIQDASLFQMANKVTSLTKNKIN
LKPNIIVLKGHNKISDFRWSRDSKRILSASQDGFMLIWDSASGLKQNAIPLDSQWVLSCAISPSTLVASAGLNNNCTIY
RVSKENRVAQNVASIFKGHTCYISDIEFTDNAHILTASGDMTCALWDIPKAKRVREYSDDLGLDVLALAIPEEPNLENSN
20 TFASCGSDGYTYIWDSRSPSAVQSFYVNDSDINALRFFKDGMSIVAGSDNGAINMYDLRSDCSIATFSLFRGYEERTPTP
TYMAANMEYNATQSPQTLKSTSSSYLDNQGAVALDFSASGRMLYSCYTDIGCVVWDVLKGEIVGKLEGHGGRVTGVRSSP
DGLAVCTGSWDSTMKIWSPGYQ

SEQ ID NO. 14

25 ste4-o17 DNA sequence (mutant)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCAACAGTATATACAACCACAAAGTCTACAGGA
TATCTCTGCAGTGGAGGAAGAAATTCAAATAAAATAGAGGCCGCCAGACAAGAGAGTAAACAGCTTCATGCTCAAATAA
ATAAAGCAAAACACAAGATACAAGATGCAAGCTTATTCCAGATGGCCAACAAAGTTACTTCGTTGACCAAAAATAAGATC
30 AACTTAAAGCCAAATATCGTGTTGAAAGGCCATAATAATAAAATCTCAGATTTTCGGTGGAGTCGAGATTCAAACGTAT
TTTGAGTGCAAGTCAAGATGGCTTTATGCTTATATGGGACAGTGCTTCAGGTTTAAACAGAACGCTATTCCATTAGATT
CTCAATGGGTTCTTTCTGCGCTATTTTCGCCATCGAGTACTTTGGTAGCAAGCGCAGGATTAAACAATAACTGTACCATT
TATAGAGTTTTCGAAAGAAAACAGAGTAGCGCAAAACGTTGCGTCAATTTTCAAAGGACATACTTGCTATATTTCTGACAT
TGAATTTACAGATAACGCACATATATTGACAGCAAGTGGGGATATGACATGTGCCTTGTGGGATATACCGAAAGCAAAGA
35 GGGTGAGAGAATATTCTGACCATTTAGGTGATGTTTTGGCATTAGCTATTCCTGAAGAGCCAAACTTAGAAAATTCCTCG
AACACATTTCGCTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCCGTCGCTGTACAAAGCTTTTA
CGTTAACGATAGTGATATTAATGCACTTCGTTTTTTCAAAGACGGGATGTCGATTGTTGCAGGAAGTGACAATGGTGCGA



NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

Nern et al.

Appl. No.: 10/054,399 Atty Docket: DYOU13.1A2CPI

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FIG. 17_E

TAAATATGTATGATTTAAGGTCGGACTGTTCTATTGCTACTTTTTCTCTTTTCGAGGTTATGAAGAACGTACCCCTACC
CCTACTTATATGGCAGCTAACATGGAGTACAATACCGCGCAATCGCCACAACTTTAAATCAACAAGCTCAAGCTATCT
AGACAACCAAGGCGTTGTTTCTTTAGATTTTAGTGCATCTGGAAGATTGATGTACTCATGCTATACAGACATTGGTTGTG
TTGTGTGGGATGTATTTAAAGGAGAGATTGTTGGAAAATTAGAAGGTCATGGTGGCAGAGTCACTGGTGTGCGCTCGAGT
5 CCAGATGGGTTAGCTGTATGTACAGGTTTCATGGGACTCAACCATGAAAATATGGTCTCCAGGTTATCAATAG

SEQ ID NO. 15

Ste4-o17 Protein sequence (mutant)

10 MAHQMDSITYSNNVTQQYIQPQSLQDISAVEEEIQNKIEAARQESKQLHAQINKAKHKIQDASLFQMAKVTSLTKNKIN
LKPNIIVLKGHNKISDFRWSRDSKRILSASQDGFMLIWDSASGLKQNAIPLDSQWVLSCAISPSSTLVASAGLNNCTIY
RVSKENRVAQNVAIFKGHTCYISDIEFTDNAHILTASGDMTCALWDIPKAKRVREYSDDLGDVLALAIPEEPNLENSN
TFASCGSDGYTYIWDSRSPSAVQSFYVNDSDINALRFFKDGMSIVAGSDNGAINMYDLRSDCSIATFSLFRGYEERTPTP
TYMAANMEYNTAQSPQTLKSTSSSYLDNQGAVSLDFSASGRMLYSCYTDIGCVVWDVLKGEIVGKLEGHGGRVTGVRSSP
15 DGLAVCTGSWDSTMKIWSPGYQ

SEQ I.D. No:16 refers to the epitope sequence "Tyr Pro Tyr Asp Val Pro Asp Tyr Ala".

SEQ I.D. No:17 refers to TEV protease recognition sequence "Gln Asn Leu Tyr Phe Gln Gly".

SEQ I.D. No:18 refers to peptide sequence "QFKLPVIAFDDLKVCKKSI".

SEQ I.D. No:19 refers to peptide sequence "QFKLPVIASGDLKVCKKSI".

SEQ I.D. No:20 refers to peptide sequence "QFKLPVIAPDDLKVCKKSI".

SEQ I.D. No:21 refers to peptide sequence "QFKLPVIASDDLKVCKKSI".

SEQ I.D. No:22 refers to peptide sequence "QYEFDVILSPELKVQMKTII".